

Application No: 10575640 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2007-08-27 08:37:14.100  
**Finished:** 2007-08-27 08:37:17.698  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 598 ms  
**Total Warnings:** 8  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 66  
**Actual SeqID Count:** 66

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

<210> 1  
<211> 78  
<212> DNA  
<213> Homo sapiens

<400> 1  
atgcgggtca cggcgcggc aaccctcata ctgctgtctt cgggagccct ggccctgacc 60  
gagacctggg ccggctcc 78

<210> 2  
<211> 26  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser  
20 25

<210> 3  
<211> 168  
<212> DNA  
<213> Homo sapiens

<400> 3  
atcggtggca ttgttgctgg cctggctgtc ctagcagttt tggtcatcg agctgtggtc 60  
gctactgtga tggtaggag gaagagctca ggtggaaaag gaggagacta ctctcaggct 120  
gcgtccagcg acagtgcaca gggctctgat gtgtctctca cagcttga 168

<210> 4  
<211> 55  
<212> PRT  
<213> Homo sapiens

<400> 4  
Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile  
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly  
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly  
35 40 45

Ser Asp Val Ser Leu Thr Ala  
50 55

<210> 5  
<211> 129  
<212> DNA  
<213> Homo sapiens

<400> 5  
cagagcaaga tgctgagtgg agtcgggggc tttgtgtgg gcctgctttt ccttggggcc 60  
gggctgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120  
ctgagctga 129

<210> 6  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu  
1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His  
20 25 30

Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser  
35 40

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Enzyme restriction site

<400> 7  
ctgcaggatcg actctagagg atcc 24

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Enzyme restriction site

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser

1 5

<210> 9

<211> 1683

<212> DNA

<213> Cytomegalovirus

<400> 9

atggagtgcg gcggtcgccg ttgtcccgaa atgatatccg tactggtcc catttcgggg 60

cacgtgctga aagccgtgtt tagtcgcggc gatacgccgg tgctgcgcga cgagacgcga 120

ctccctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatgcag 180

tacacgccccg actcgacgcc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg 240

tactttacgg gcagcgaggt ggagaacgtg tcggtaaacc tgccacaaccc cacggggcga 300

agcatctgcc ccagccagga gccccatgtcg atctatgtgt acgcgcgtgcc gctcaagatg 360

ctgaacatcc ccagcatcaa cgtgcaccac taccctgtcg cggccgagcg caaacaccga 420

cacctgccccg tagctgacgc tggattcac gcgtcgccca agcagatgtg gcaggcgctg 480

ctcacggctc cgggactggc ctggacgcgt cagcagaacc agtggaaaga gccccacgtc 540

tactacacgt cagcggtcggt gtttcccacc aaggacgtgg cactgcggca cgtgggtgtgc 600

gcgcacgagc tgggttgctc catggagaac acgcgcgcac ccaagatgca ggtgataggt 660

gaccagtacg tcaagggtgta cctggagtcc ttctgcgagg acgtgcgcctc cggcaagctc 720

tttatgcacg tcacgctggg ctctgacgtg gaagaggacc tgacgatgac ccgcaacccg 780

caacccttca tgcgccccca ctagcgcaac ggcttacgg tgggtgtcc caaaaatatg 840

ataatcaaac cggcaagat ctgcacatc atgctggatg tggctttac ctcacacgag 900

cattttgggc tgctgtgtcc caagagcatc cggggcctga gcatctcagg taacctgttg 960

atgaacgggc agcagatctt cctggaggtt caagccatac gcgagaccgt ggaactgcgt 1020

cagtagcata cctgggtgtgc gctttttttt ttcgatatacg acttgctgtct gcaagcgccgg 1080

cctcagtagaca gcgagcaccc cacttcacc agccagatcc gcatccagg caagctttag 1140

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accagcgat cggactccga cgaagaactc gtaaccaccc agcgcaagac gccccgcgtc 1260

accggcgccg gcgccatggc gggcgccctcc acttccgcgg gccgcaaaccg caaatcagca 1320

tcctcggcga cggcgtgcac gtcgggctttt atgacacgcg gccgccttaa ggcggagtcc 1380

accgtcgcc ccgaagagga caccgacgag gattccgaca acgaaatcca caatccggcc 1440  
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gg 1683

<210> 10  
<211> 561  
<212> PRT  
<213> Cytomegalovirus

<400> 10

Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly  
1 5 10 15

Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr  
20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val  
35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp  
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr  
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn  
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr  
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val  
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val  
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg  
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys  
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp  
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met  
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val  
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu  
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met  
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe  
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser  
275 280 285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu  
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu  
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr  
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Asp  
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr  
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr

370

375

380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp  
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys  
405 410 415

Thr Pro Arg Val Thr Gly Gly Ala Met Ala Gly Ala Ser Thr Ser  
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser  
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro  
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala  
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu  
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu  
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu  
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln  
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg  
545 550 555 560

Gly

<210> 11

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid encoding a fusion protein

<400> 11  
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cgccgttgc cggaaatgat atccgtactg ggtcccattt cggggcacgt gctgaaagcc 180  
gtgttagtc gcgcgatac gcccgtgctg cgcacgaga cgcgactct gcagacgggt 240  
atccacgtac gcgtgagcca gcccgtgctg atcttggat cgcagtacac gcccgtactg 300  
acgcatgcc accgcggcga caatcagctg caggtgcagc acacgtactt tacgggcagc 360  
gaggtggaga acgtgtcggt caacgtgcac aacccacgg gccgaagcat ctgccccagc 420  
caggagccca tgtcgatcta tgtgtacgctg ctgcccgtca agatgtgaa catccccagc 480  
atcaacgtgc accactaccc gtcggggcc gagcgcacaa accgacacct gcccgtagct 540  
gacgctgtga ttcacgcgtc gggcaagcag atgtggcagg cgcgtctcac ggtctcggt 600  
ctggcctggc cgcgtcagca gaaaccagtgg aaagagcccg acgtctacta cacgtcagcg 660  
ttcgtgtttc ccaccaagga cgtggactg cggcacgtgg tgtgcgcgca cgagctggtt 720  
tgctccatgg agaacacgcg cgcaccaag atgcaggtga taggtgacca gtacgtcaag 780  
gtgtacctgg agtccttctg cgaggacgtg ccctccggca agcttttat gcacgtcacg 840  
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ccccacgagc gcaacggctt tacgggtttg tgtccaaaa atatgataat caaaccgggc 960  
aagatctcgc acatcatgtt ggtatgtggct ttacccatc acgagcattt tgggtgttg 1020  
tgtcccaaga gcatccggg cctgagcata tcaggttaacc tggatgtgaa cgggcagcag 1080  
atcttcctgg aggtacaagc catacgcgag accgtggaac tgcgtcagta cgatccctgg 1140  
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gaggacacccg acgaggattc cgacaacgaa atccacaatc cggccgtgtt cacctggccg 1560  
ccctggcagg cggcatcct ggcccgcaac ctgggtcccc tggtggtac gttcagggt 1620

cagaatctga agtaccagga attcttctgg gacgccaacg acatctaccg catttcgcc 1680  
gaatttggaaag gcgtatggca gcccgtgcg caacccaaac gtcggcccca cccggcaagac 1740  
gccttgccccg ggccatgcat cgcctcgacg cccaaaaagc accgaggtgg atccatcgta 1800  
ggcattgttg ctggcctggc tgccttagca gttgtggtca tcggagctgt ggtcgctact 1860  
gtgatgtgtta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc 1920  
agcgacagtg cccagggctc tgatgtgtct ctcacagctt ga 1962

<210> 12  
<211> 653  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion protein

<400> 12

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala  
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg  
20 25 30

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser  
35 40 45

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg  
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly  
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr  
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val  
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn  
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met  
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser  
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His  
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp  
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn  
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro  
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val  
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp  
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser  
260 265 270

Gly Lys Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp  
275 280 285

Leu Thr Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg  
290 295 300

Asn Gly Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly  
305 310 315 320

Lys Ile Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His  
325 330 335

Phe Gly Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly  
340 345 350

Asn Leu Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile  
355 360 365

Arg Glu Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe  
370 375 380

Phe Phe Asp Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu  
385 390 395 400

His Pro Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr  
405 410 415

Arg His Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp  
420 425 430

Asp Val Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr  
435 440 445

Glu Arg Lys Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala  
450 455 460

Ser Thr Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala  
465 470 475 480

Cys Thr Ser Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr  
485 490 495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His  
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala  
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys  
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala  
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg  
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys  
580 585 590

Lys His Arg Gly Gly Ser Ile Val Gly Ile Val